Genetic clusters and circulation of Salmonella Dublin in Jutland

de Knegt, Leonardo Victor; Kudirkiene, Egle; Sørensen, Gitte; Nielsen, Liza R.; Olsen, John E.

Publication date:
2017

Document Version
Publisher's PDF, also known as Version of record

FACULTY OF HEALTH AND MEDICAL SCIENCES
UNIVERSITY OF COPENHAGEN

Genetic clusters and circulation of *Salmonella* Dublin in Jutland

Leonardo V. de Knegt[1], Egle Kudirkiene[1], Gitte Sørensen[2], Liza R. Nielsen[1], John E. Olsen[1]

[1] Department of Veterinary and Animal Sciences, University of Copenhagen, Denmark, leonardo@sund.ku.dk

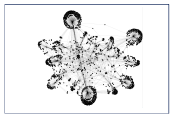
[2] National Food Institute, Technical University of Denmark / Statens Serum Institut, Denmark

BACKGROUND

2002: Danish *S.* Dublin surveillance program
2007: National eradication programme initiated
2010: Enforced trade restrictions in legislation
2013: Mandatory control and strict trade restrictions

CHALLENGE

Continued circulation of *S.* Dublin, but cattle movements too intricate to detect clear circulation patterns based on existing data. Many herds interconnected by 1st or 2nd or higher degree contacts



OBJECTIVE

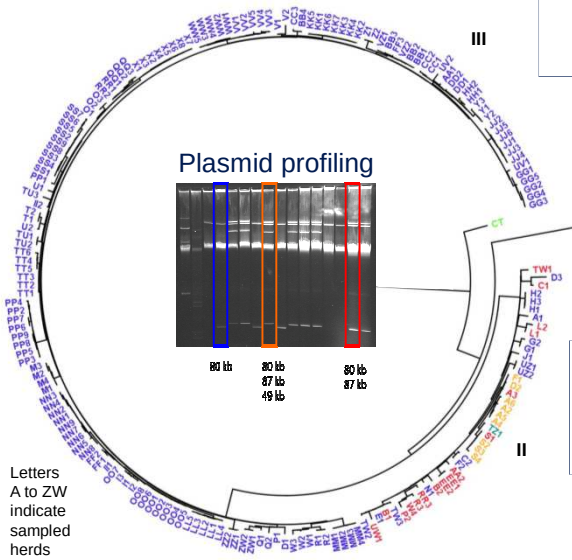
To use whole genome sequencing (WGS) to improve the understanding of strain circulation between herds

METHODS

- *S.* Dublin: 197 isolates from 58 herds 1996 to 2016
- Sequencing: MiSeq 250 bp pair-end
- Assembly/Annotation: SPADEs 3.9.1./Prokka 1.0
- Population structure analysis: CSI Phylogeny
- Genome content analysis: Roary/Scoary
- Movement of cattle between herds since 1994: from Danish Cattle Database

RESULTS

Core genome clusters



Letters A to ZW indicate sampled herds

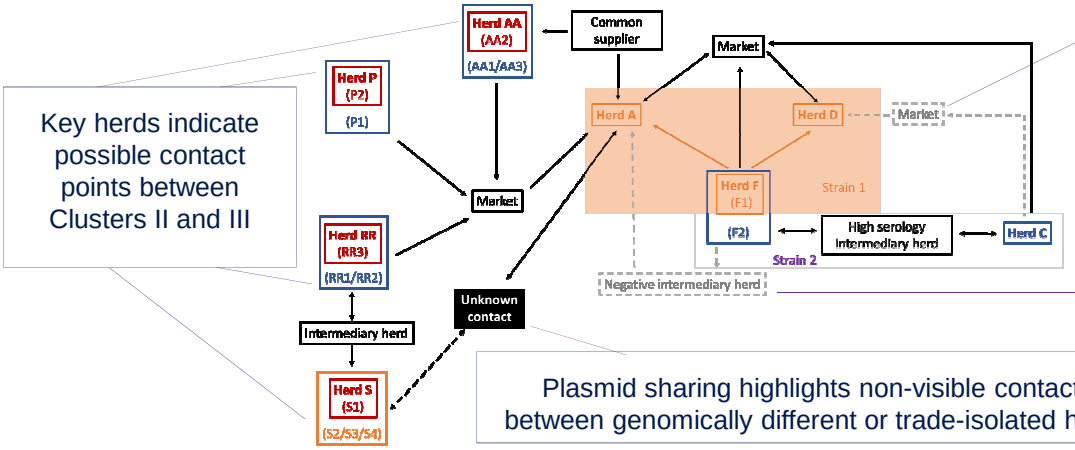
Cluster III
Mid- and South Jutland

Cluster I
highly distant, may be ancestral Danish strains

Cluster II
mostly North, heavily enriched by plasmids

Location of herds by cluster and plasmid profile (colours)

Example of movement network



Trade network centered around markets

Key herds indicate possible contact points between Clusters II and III

Core genome differences discard false circulation nodes

Serology helps discard negative intermediaries

Plasmid sharing highlights non-visible contacts between genomically different or trade-isolated herds

The study was funded by The Danish Agriculture Levy Fund